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Fig. 1

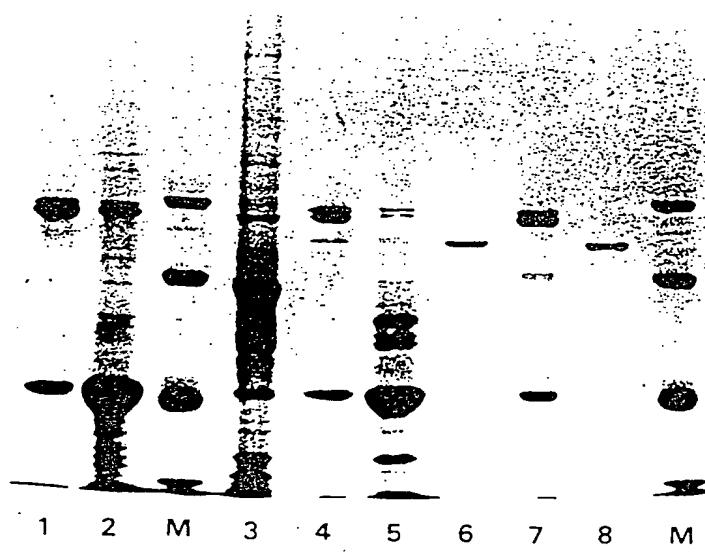


Fig. 2

adseverin C39 K V A H V K Q I P F D A
gelsolin 386 H I A N V E R V P F D A
villin 365 K V A K V E Q V K F D A

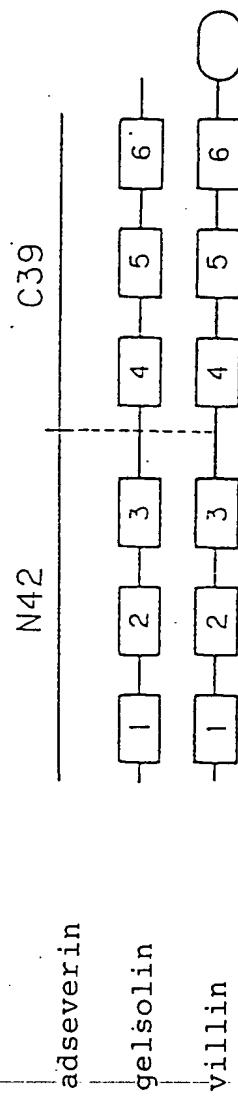


Fig. 3

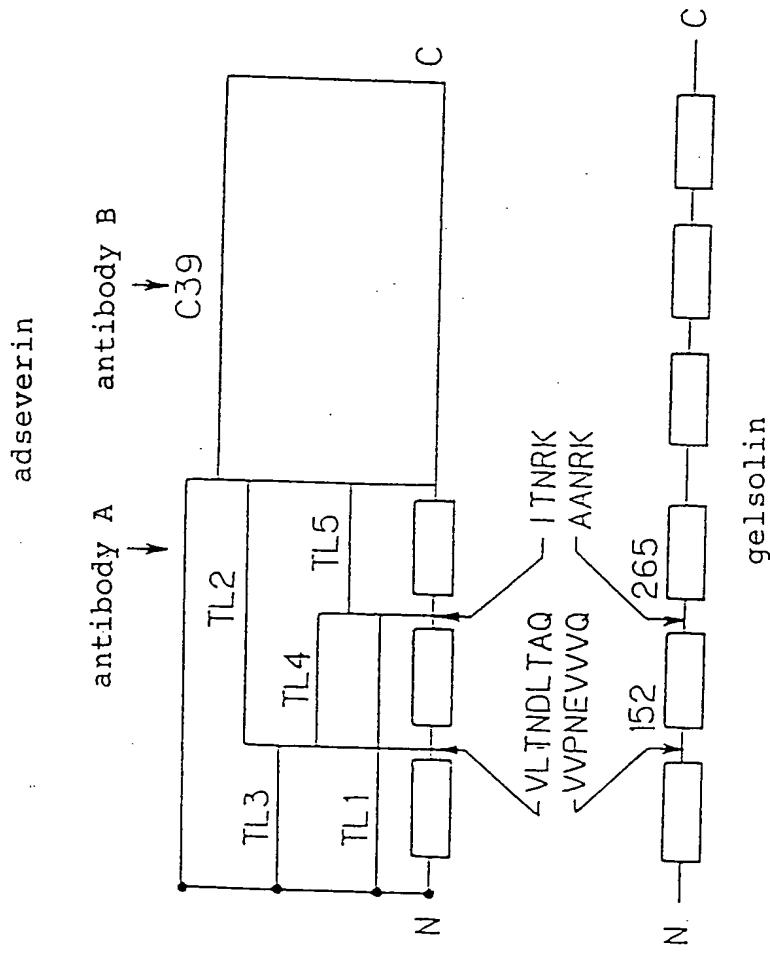


Fig. 4

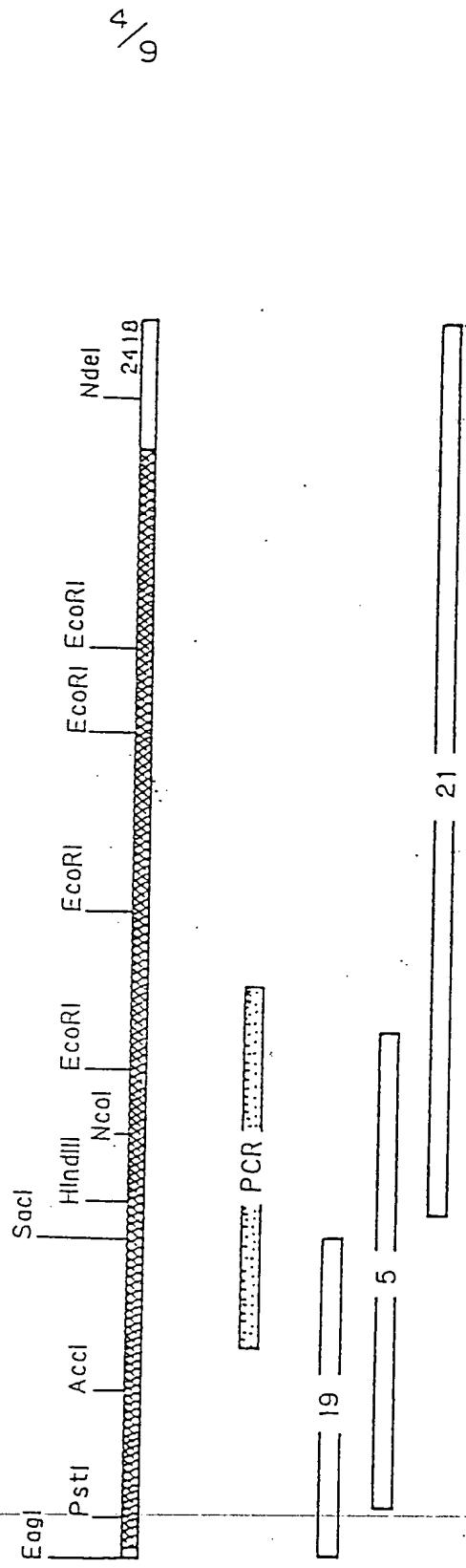


Fig. 5A

ADS	008	EEFAR-AGK-R	AGLQVWRIE	KLELVPVPESAYGN	
GEL	057	PEFLK-AGK-E	PGIQIWRVE	KFDLVPVPPTNLYGD	1
VIL	007	QVKGS-LNITT	PGLQIWRIE	AMQMVPVPSTSFGS	
ADS	385	AAQHHWVDDGS	GVQOIWRVE	NNGRVEIDRNSYGE	
GEL	434	AAQHGMDDGT	GQKQIWRIE	GSNKVPVDPATYGO	4
VIL	387	AAQQKMWDDGS	GEVQVWRIE	NLELVVPVDSDKWLGH	
ADS	127	NHVLTNDLTAQ	RLLHVKGRR	-VV RATE VPISWDS	
GEL	177	KHWVPNEVVQ	RLFQVKGRR	-VV RATE VPWSWES	2
VIL	127	KHVETNSYDVQ	RLLHVKGRR	NVV-A GEV EMSWKS	
ADS	503	GQAPAPPI--RI	FQVRNLAS	I TRIM-EVDVDANS	
GEL	556	GOTAPAST--RI	FQVRANSAG	ATRAV-EVLKAGA	5
VIL	508	NLETGPST--RI	FQVQGTGAN	NTKAF-EVPARANF	
ADS	245	NRKMAK-LYMV	SDASGSMKV	SLVAEENPFSMAM	
GEL	294	NRKLAK-LYKV	SNGAGTMSV	SLVADENPFAQGA	3
VIL	250	KAAL-K-LYHV	SDSEGNLTVV	REVAT-RPLTQDL	
ADS	610	ED-HPPRLYGC	SNKTGRFTI	EEVPGE--FTQDD	
GEL	662	MDAHPRLFAC	SNKIGRFVI	EEVPGE--IMQED	6
VIL	615	LVI-TPRLFEC	SNKTGRFLA	TEIP-D--FNQDD	

Fig. 5B

ADS	F	YVG	D	A	YLV	LHTTQASRG---FTYR	L	HF	W	L	G	KECTQD	E	STA	A	1
GEL	F	FTG	D	A	YVI	LKTQQLRNGN--LQYD	L	HY	W	L	G	NECSQD	E	SGA	A	
VIL	F	FDG	D	C	YII	LAIH--KTASS-LSYD	I	HY	W	I	G	QDSSLD	E	QGA	A	
ADS	F	YGG	D	C	YII	LYTYPR----GQI---	I	YT	W	Q	G	ANATRD	E	LTT	S	
GEL	F	YGG	D	S	YII	LYNYRHGGRQGQI---	I	YN	W	Q	G	AQSTQD	E	VAA	S	
VIL	F	YGG	D	C	YLL	LYTYLIGEKQHYL---	L	YV	W	Q	G	SQASQD	E	ITA	S	
ADS	F	NKG	D	C	FI	-----DLGTE	I	YQ	W	C	G	SSCNKY	E	RLK	A	
GEL	F	NNG	D	C	FI	-----DLGN	I	HQ	W	C	G	SNSNRY	E	RLK	A	2
VIL	F	NRG	D	V	FLL	-----DLGKL	I	IQ	W	N	G	PESTRM	E	RLR	G	
ADS	L	NSN	D	V	FVL	-----KLRQNN	G	YI	W	I	G	KGSTOE	E	EKG	A	
GEL	L	NSN	D	A	FVL	-----KT-PSA	A	YL	W	V	G	TGASEA	E	KTG	A	3
VIL	L	NSN	D	V	FVL	-----KT-QSC	C	YL	W	C	G	KGC SGD	E	REM	A	
ADS	L	LSE	E	C	FIL	-----DHGAAKQ	I	FV	W	K	G	KDANPQ	E	RKA	A	
GEL	L	KSE	D	C	FIL	-----DHGKDGR	I	FV	W	K	G	KQANTE	E	RKA	A	
VIL	L	SHE	D	C	YIL	-----DQG-GLK	I	YY	W	K	G	KKANEQ	E	KKG	A	4
ADS	L	AED	D	V	MLL	-----DAWEQ	I	FI	W	I	G	KDANEV	E	KSE	S	
GEL	L	ATD	D	V	MLL	-----DTWDO	V	FV	W	V	G	KDSQEE	E	KTE	A	
VIL	L	EED	D	V	FLL	-----DVWDO	V	FF	W	I	G	KHANE	E	KK	A	5

◀ Motif B ▶

◀ Motif A ▶

Fig. 5C

ADS	AIFTVQMDDYLGKPVQNREL---	QG	Y	ES	TD	FV	G	YF	1
GEL	AIFTVQLDDYLNGRAVQHREV---	QG	F	ES	AT	FL	G	YF	
VIL	AIYTQMDDFLKGRAVQHREV---	QG	N	ES	EA	FR	G	YF	
ADS	AFLTQQLDRSLGGQAVQIRVS---	QG	K	EP	AH	LL	S	LF	4
GEL	AILTAQLDEELGGTPVQSRVV---	QG	K	EP	AH	LM	S	LF	
VIL	AYQAVILDQKYNGEPVQIRVP---	MG	K	EP	PH	LM	S	IF	
ADS	SQVAIGIRDNERKGRAQLIVVE---	EG	S	EP	SE	LT	K	VL	
GEL	TQVSKGIRDNERSGRARVHVE---	EG	T	EP	EA	ML	Q	VL	2
VIL	MTLAKEIRRDQERGGRTYVGVDGEN	EL	A	SP	-K	LM	E	VM	
ADS	EYVASVL-----KCKTSTIQ---	EG	K	EP	EE	FW	N	SL	
GEL	QELLRLV-----RAQPVQVA---	EG	S	EP	DG	FW	E	AL	
VIL	KMVADTISRTEK-----QV-VW----	EG	Q	EP	AN	FW	M	AL	
ADS	MKTAEEFLQQMNYSTNT-QIQVLP-	EG	G	ET	P	IF	KQ	FF	
GEL	LKTASDFITKMDYPKQT-QVSVLP-	EG	G	ET	P	LF	KQ	FF	
VIL	MSHALNFIKAKOYPYST-QVEVON-	DG	A	ES	A	VF	QQ	LF	
ADS	LKSAKIYLETDPSGRDKRTPIVIK	QG	H	EP	PT	FT	GW	FL	3
GEL	ITSAKRYIETDPANRDRRTPTIVVK	QG	F	EP	PS	FV	GW	FL	
VIL	ATTAAQEYLIKTHPSGRDPETPIIVVK	QG	H	EP	PT	FT	GW	FL	6

↑ Motif C ↓

Fig. 5D

ADS	-	KGGIKY---KA	GGVASGL	126	
GEL	-	KSGLKY---KK	GGVASGF	176	
VIL	-	KQGLVI---RK	GGVASSGM	126	1
ADS	-	---KDKPLIIY	KNGTSKKE	502	
GEL	-	---GGKPMIY	GGGTSREG	555	
VIL	-	---KGR-MVVY	QGGTSRTN	507	4
ADS	-	---GEKPKL RD	GEDDDDIKADIT	244	
GEL	-	---GP KPALPA	GTEDTA-KEDAA	293	
VIL	N	HVLGKRRELKA	AVPDTV-VEPAL	249	2
ADS	-	---GGK---KD	YQTS-PLLESQA	609	
GEL	-	---GGK---AA	YRTS-PRLKDKK	661	
VIL	-	---GGK---AP	YANT-KRLQEEN	614	5
ADS	K	DWRDRDQSDGF	GKVYVTEKVAH	367	
GEL	K	NWRDPDQT DGL	GLSYLSSHIAN	416	
VIL	Q	KWTASNRTSGL	GKTHTVGSVAK	369	3
ADS	G	WDSSRW		715	
GEL	G	WDDDYWSVDPL	-DRAMAEAA	782	
VIL	A	WDPFKWSNTKS	YEDLKAESGN	734	6

Fig. 5E



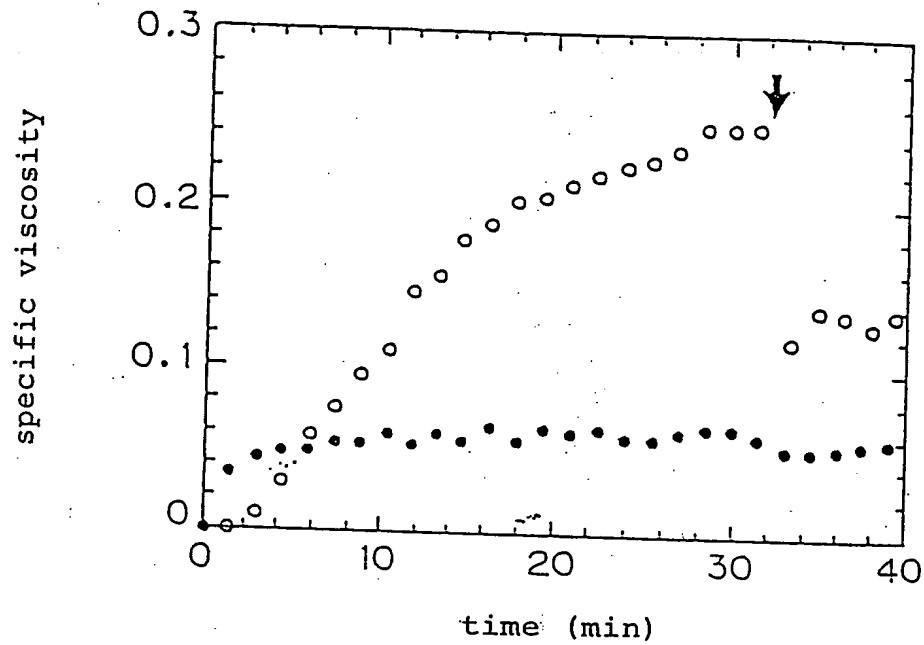
Fig. 6



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Fig. 7

A



B

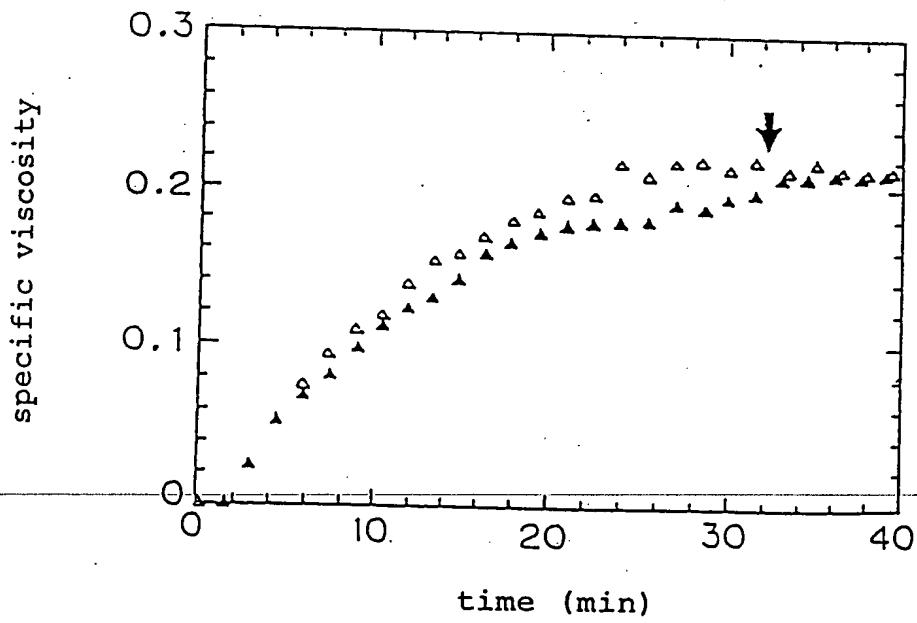


Fig. 8

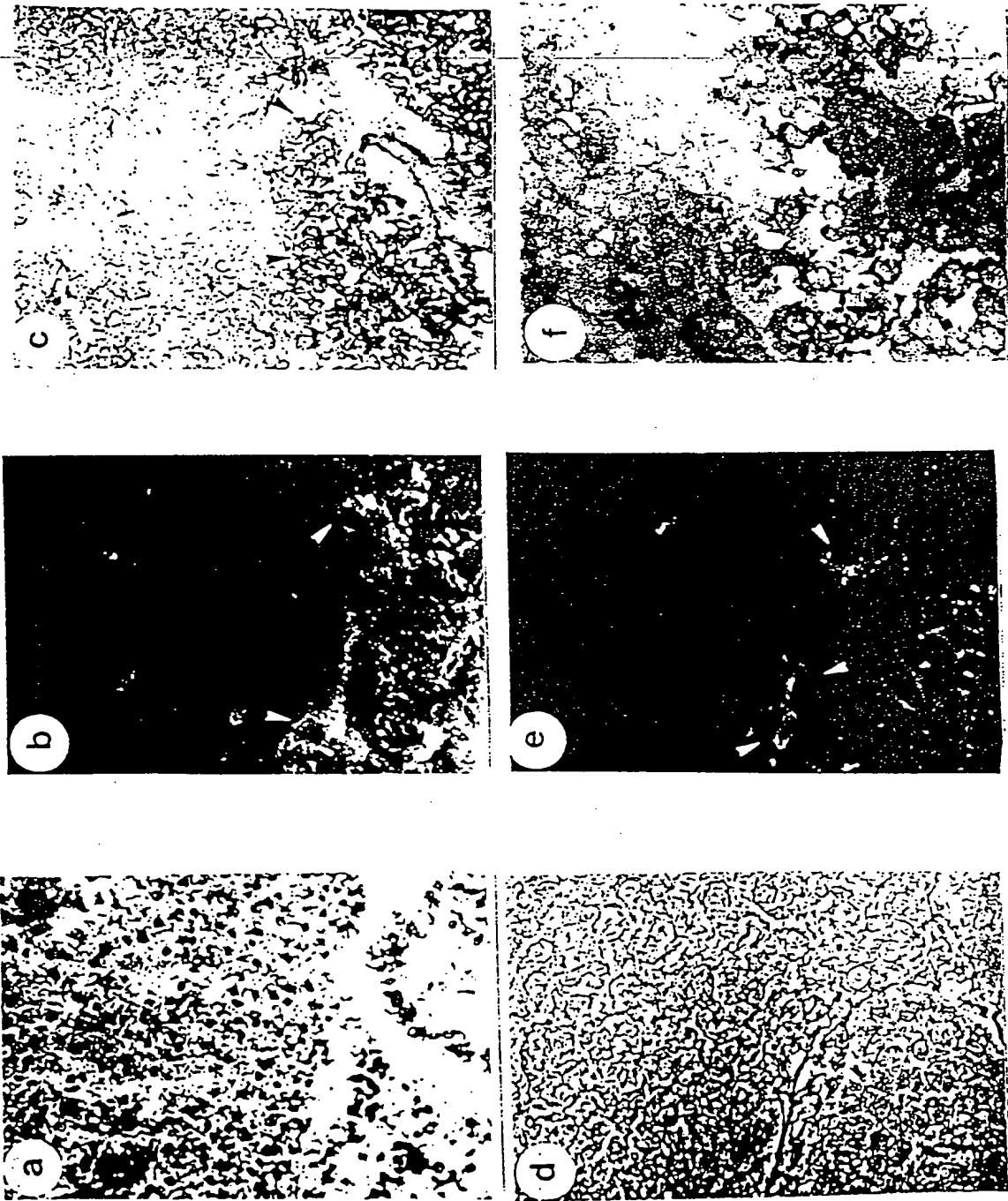


Fig. 9

1' MARELYHEEFARAGKQAGLQVWRIEKLELYPVPOSAHGDFYVGDAYVLHTAKTSRGFTY

1" MAQGLYHEEFARAGKRALQVWRIEKLELYPVPEAYGNFYVGDAYVLHTTQASRGFTY

61' HLHFWLKGKECSQDESTAAAIFTVQMDOYLGGKPVNRELQGYESNOFVSYFKGGLKYKAG

61" RLHFWLKGKECTQDESTAAAIFTVQMDOYLGGKPVNRELQGYESTDFVGYFKGGLKYKAG

121' GVASGLNHVLTNDLTAKRLLHVGRMVRATEVPLSWDSFNKGDCFIIDLGEIYQWCGS

121" GVASGLNHVLTNDLTACRLLHVGRMVRATEVPLSWDSFNKGDCFIIDLGEIYQWCGS

181' SCNKYERLKAQVATGIRYNERKGRSELIWEEGSEPSLIKVLGEKPELPOGGDOOOII

181" SCNKYERLKASQVAIGIRONERKGRAQLIVVEEGSEPSELTKVLGEKPKLROGEDOOOI

241' ADISNRKMAKLYMSDASGSMRVTVAAEENPFSMALLSEECFILDHGAAKQIFVWKGD

241" ADITNRKMAKLYMSDASGSMKVSLVAEENPFSMALLSEECFILDHGAAKQIFVWKGD

301' ANPQERKAAMKTAEEFLQQMNYSKNTQIQVLPEGGETPIFKQFFKDWRDKDQSDGFGKVVY

301" ANPQERKAAMKTAEEFLQQMNYSTNTQIQVLPEGGETPIFKQFFKDWRDRDQSDGFGKVVY

361' VTEKVAQIKQIPFDASKLHSPPQMAAQHNMDOGSGKVEIWRENNGRIQVDQNSYGEFY

361" VTEKVAHKQIPFDASKLHSPPQMAAQHHYDOGSGKVOIWRENNGRVEIDRNSYGEFY

421' GGDCYIILYTYPRGQIIYTQGANATROELTSAFLTVQLDRLGGQAVQIRVSQGKEPV

421" GGDCYIILYTYPRGQIIYTQGANATROELTSAFLTVQLDRLGGQAVQIRVSQGKEPA

481' HLLSLFKDKPLIIYKNGTSKKGGQAPAPPTRLFQVRRNLASITRIVEVDVDANSLSNOV

481" HLLSLFKDKPLIIYKNGTSKKEGQAPAPPRLFQVRRNLASITRIMEVDVDANSLSNOV

541' CVLKLQPQNSGYIWVGKGASQEEKGAEYVASVLCKTLRIQEGEREEPEFHNSLGGKKDYQ

541" FVLKLRQNNGYIWIGKGSTQEEKGAEYVASVLCKTSTIQEGEREEPEFHNSLGGKKDYQ

601' TSPLLETQAEDHPPRLYGCNSKTGRFVIEEIPGEFTQ00LAEDOVMLLDAWEQIFIWIGK

601" TSPLLESQAEDHPPRLYGCNSKTGRFVIEEVPGEFTQ00LAEDOVMLLDAWEQIFIWIGK

661' DANEVEKKESSLKSAKMYLETOPSGRDKRTPIVIICKQGHEPPTFTGWFLGWSSKW

661" DANEVEKSESLKSAKIYLETOPSGRDKRTPIVIICKQGHEPPTFTGWFLGWSSRW